PCT10

RAW SEQUENCE LISTING   DATE: 12/11/2002 *P-6*
PATENT APPLICATION: **US/10/070,240A**   TIME: 09:34:59

Input Set : **N:\Crf4\11252002\J070240.raw**
Output Set: **N:\CRF4\12112002\J070240A.raw**

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 1 <110> APPLICANT: WATANABE, TAKUYA
 2        TERAO, YASUKO
 3        SHINTANI, YASUSHI
 4 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
 5        THEREOF
 6 <130> FILE REFERENCE: (46342) 57127
 7 <140> CURRENT APPLICATION NUMBER: US/10/070,240A
 8 <141> CURRENT FILING DATE: 2002-02-27
 9 <150> PRIOR APPLICATION NUMBER: JP 2000-217474
10 <151> PRIOR FILING DATE: 2000-07-18
11 <150> PRIOR APPLICATION NUMBER: JO 11-241531
12 <151> PRIOR FILING DATE: 1999-08-27
13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05685
14 <151> PRIOR FILING DATE: 1999-08-27
15 <160> NUMBER OF SEQ ID NOS: 34
16 <170> SOFTWARE: PatentIn Ver. 2.1
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20 <212> TYPE: PRT
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26                    20                  25                  30
27     Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
28                35                  40                  45
29     Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
30          50                  55                  60
31     Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn
32      65                  70                  75                  80
33     Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
34                    85                  90                  95
35     Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
36                   100                 105                 110
37     Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
38                   115                 120                 125
39     Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
40          130                 135                 140
41     Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
42     145                 150                 155                 160
43     Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
44                   165                 170                 175
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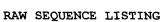
RAW SEQUENCE LISTING   DATE: 12/11/2002
PATENT APPLICATION: **US/10/070,240A**   TIME: 09:34:59

Input Set : **N:\Crf4\11252002\J070240.raw**
Output Set: **N:\CRF4\12112002\J070240A.raw**

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47        Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
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49        Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
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51        Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
52        225                 230                 235                 240
53        Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
54                    245                 250                 255
55        Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
56                    260                 265                 270
57        Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
58                    275                 280                 285
59        Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
60              290                 295                 300
61        Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
62        305                 310                 315                 320
63        Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
64                    325                 330                 335
65        Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
66                    340                 345                 350
67        Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
68              355                 360                 365
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77 <213> ORGANISM: Homo sapiens
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85        acc agc ttc ctt tct gtg ctc aac cct cat gga gcc cat gcc act tcc    96
86        Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala Thr Ser
87                     20                  25                  30
88        ttc cca ttc aac ttc agc tac agc gac tat gat atg cct ttg gat gaa   144
89        Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
90                     35                  40                  45
91        gat gag gat gtg acc aat tcc agg acg ttc ttt gct gcc aag att gtc   192
92        Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
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 97      ttc atc ttt atc gct gcc ctg gtc cgc tac aag aaa ctg cgc aac ctc   288
 98      Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
 99                       85              90              95
100      acc aac ctg ctc atc gcc aac ctg gcc atc tct gac ttc ctg gtg gcc   336
101      Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
102                      100             105             110
103      att gtc tgc tgc ccc ttt gag atg gac tac tat gtg gtg cgc cag ctc   384
104      Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
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106      tcc tgg gag cac ggc cac gtc ctg tgc acc tct gtc aac tac ctg cgc   432
107      Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
108                      130             135             140
109      act gtc tct ctc tat gtc tcc acc aat gcc ctg ctg gcc atc gcc att   480
110      Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
111      145             150             155             160
112      gac agg tat ctg gct att gtc cat ccg ctg aga cca cgg atg aag tgc   528
113      Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
114                      165             170             175
115      caa aca gcc act ggc ctg att gcc ttg gtg tgg acg gtg tcc atc ctg   576
116      Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu
117                      180             185             190
118      atc gcc atc cct tcc gcc tac ttc acc acc gag acg gtc ctc gtc att   624
119      Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
120                      195             200             205
121      gtc aag agc cag gaa aag atc ttc tgc ggc cag atc tgg cct gtg gac   672
122      Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
123                      210             215             220
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125      Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
126      225                     230             235             240
127      ttc gtg ggc ccc gtg gtc acc atg acc ctg tgc tat gcc agg atc tcc   768
128      Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
129                      245             250             255
130      cgg gag ctc tgg ttc aag gcg gtc cct gga ttc cag aca gag cag atc   816
131      Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
132                      260             265             270
133      cgc aag agg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc   864
134      Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
135                      275             280             285
136      atc ctc acc gcc tac gtg cta tgc tgg gcg ccc ttc tac ggc ttc acc   912
137      Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
138                      290             295             300
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140      Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
141      305                     310             315             320
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143      Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
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150                     355              360              365
151     aag tcc agt gca gac ctg gac ctc aag aca att ggg atg cct gcc acc    1152
152     Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
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158 <210> SEQ ID NO: 3
159 <211> LENGTH: 1179
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
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163 <221> NAME/KEY: CDS
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169     acc agc ttc ctt tct gtg ctc aac cct cat gga gcc cat gcc act tcc    96
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171                     20               25               30
172     ttc cca ttc aac ttc agc tac agc gac tat gat atg cct ttg gat gaa    144
173     Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
174                     35               40               45
175     gat gag gat gtg acc aat tcc agg acg ttc ttt gct gcc aag att gtc    192
176     Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
177         50               55               60
178     att ggg atg gcc ctg gtg ggc atc atg ctg gtc tgc ggc att gga aac    240
179     Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn
180      65               70               75               80
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183                     85               90               95
184     acc aac ctg ctc atc gcc aac ctg gcc atc tct gac ttc ctg gtg gcc    336
185     Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
186                     100              105              110
187     att gtc tgc tgc ccc ttt gag atg gac tac tat gtg gtg cgc cag ctc    384
188     Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
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190     tcc tgg gag cac ggc cac gtc ctg tgc acc tct gtc aac tac ctg cgc    432
191     Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
192         130              135              140
193     act gtc tct ctc tat gtc tcc acc aat gcc ctg ctg gcc atc gcc att    480
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196        gac agg tat ctg gct att gtc cat ccg ctg aga cca cgg atg aag tgc    528
197        Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
198                        165                 170                 175
199        caa aca gcc act ggc ctg att gcc ttg gtg tgg acg gtg tcc atc ctg    576
200        Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu
201                        180                 185                 190
202        atc gcc atc cct tcc gcc tac ttc acc acc gag acg gtc ctc gtc att    624
203        Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
204                        195                 200                 205
205        gtc aag agc cag gaa aag atc ttc tgc ggc cag atc tgg cct gtg gac    672
206        Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
207                210                 215                 220
208        cag cag ctc tac tac aag tcc tac ttc ctc ttt atc ttt ggc ata gaa    720
209        Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
210        225                 230                 235                 240
211        ttc gtg ggc ccc gtg gtc acc atg acc ctg tgc tat gcc agg atc tcc    768
212        Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
213                        245                 250                 255
214        cgg gag ctc tgg ttc aag gcg gtc cct gga ttc cag aca gag cag atc    816
215        Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
216                        260                 265                 270
217        cgc aag agg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc    864
218        Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
219                275                 280                 285
220        atc ctc acc gcc tac gtg cta tgc tgg gcg ccc ttc tac ggc ttc acc    912
221        Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
222                290                 295                 300
223        atc gtg cgc gac ttc ttc ccc acc gtg ttt gtg aag gag aag cac tac    960
224        Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
225        305                 310                 315                 320
226        ctc act gcc ttc tac atc gtc gag tgc atc gcc atg agc aac agc atg    1008
227        Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
228                        325                 330                 335
229        atc aac act ctg tgc ttc gtg acc gtc aag aac gac acc gtc aag tac    1056
230        Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
231                        340                 345                 350
232        ttc aaa aag atc atg ttg ctc cac tgg aag gct tct tac aat ggc ggt    1104
233        Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
234                355                 360                 365
235        aag tcc agt gca gac ctg gac ctc aag aca att ggg atg cct gcc acc    1152
236        Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
237                370                 375                 380
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240        385                 390
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 31
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/11/2002
PATENT APPLICATION: **US/10/070,240A**   TIME: 09:35:00

Input Set : **N:\Crf4\11252002\J070240.raw**
Output Set: **N:\CRF4\12112002\J070240A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 7,13
Seq#:31; Xaa Pos. 7

VERIFICATION SUMMARY   DATE: 12/11/2002
PATENT APPLICATION: **US/10/070,240A**   TIME: 09:35:00

Input Set : **N:\Crf4\11252002\J070240.raw**
Output Set: **N:\CRF4\12112002\J070240A.raw**

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L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0